

Table 1. Identification of peptides in AfC fractions.

Protein extract	Cssl (AnrP440134)	Hydrophobin (AnrP57221)	GAPDH (AnrP539502)	Enolase (AnrP7789)	Catalases and IMDH B
Diffusate	KVAQEIINPGPK	FPVPDDITVK ATYAADVTDIDEGLIAGTLK	AGISLNPNFVK TAAQNIIIPSSGAAK NILGYTEDDVVSSDLNGDER	NVNETIGPALIK VNQIGTITFESIQA TSDFOIVGDDDLTVTNPGR	Not detected
Cell surface exposed	VAQEIINPGPK	FPVPDDITVK ATYAADVTDIDEGLIAGTLK	Not detected	WLTYEQIADLYK Not detected	FGFDLLDPTK (Catalase B peptide AnrP977704) LX ₁ AEX ₂ ALR (IMDH B peptide)
Cell wall	KVAQEIINPGPK VAQEIINPGPK SISFQIDCR EGAEOQAPQAEHSTK VVTTPYTCDOVK	FPVPDDITVK 3-12 ATYAADVTDIDEGLIAGTLK 30-50	AGISLNPNFVK TAAQNIIIPSSGAAK NILGYTEDDVVSSDLNGDER VPTSNSVVDLTCR YDTTHGQFK	Not detected	TGPSLLEDQIAR (Catalase A peptide AnrP145557)
Peptides used for Ab production	KVAQEIINPGPKVVT KEGAEOQAPQAEHSTK	PVPDDITVKQATEKCGD ATYAADVTDIDEGLI	GTIETYYDQGLIVNGK TEDDVVSSDLNGDERS FKGTIETYYDQGLIVNGKK	KNVNETIGPALIKENID TSDFOIVGDDDLTVTNPGR	DEEDQILRFGFDLLDPTKIIVP RIDNDLARRVARAIGV

Table 2. Biochemical characteristics of Csl.

	Complete	N-terminus	C-terminus
MW	28179.92	13960.38	14236.54
Residues	260	130	130
Strongly Basic (+) Amino Acids (K, R)	25	10	15
Strongly Acidic (-) Amino Acids (D, E)	33	9	24
Hydrophobic Amino Acids (A, I, L, F, W, V)	89	55	34
Polar Amino Acids (N, C, Q, S, T, Y)	70	36	34
Isoelectric Point	5.081	7.626	4.760
Charge at pH 7.0	-7.634	0.892	-8.617

Table 3. Sequence of peptides chosen for the production of multiple antigenic peptides and antisera against selected target proteins

<u>Peptide name</u>	<u>Peptide sequence</u>	<u>Parental protein</u>	<u>Reactivity vs AfC*</u>	<u>Reactivity vs AfM*</u>
GAP-B-1	FKGTLETYDQGLVNGKK (SEQ ID NO:12)	GAPDH B	++	+++
GAP-B-2	TEDDVVSDDLNGDERS (SEQ ID NO:11)	GAPDH B	+++	++
HYD-1	PVPDDITVKQATEKCGD (SEQ ID NO:9)	hydrophobin	++	+++
HYD-2	ATYAGDVTDDIEGIL (SEQ ID NO:10)	hydrophobin	++	+
CAT-B-1	DEBDQLRFGFDLDP TKIVP (SEQ ID NO:15)	Catalase B	++	++
CAT-B-2	RIDNDLARRVARAIGV (SEQ ID NO:16)	Catalase B	++	++
ENO-1	KNVNETITGPALIKENID (SEQ ID NO:13)	Enolase	++	-
ENO-2	TSDFQIVGDDLTVTNPGR (SEQ ID NO:14)	Enolase	-	+
Peptide 2	KEGAEQSAPQAEHSTK (SEQ ID NO:8)	CssI	+++	+++
Peptide 1	KVAQEIIINPGPKVVTT (SEQ ID NO:7)	CssI	++	++

*Reactivity of sera raised against the peptide against the surface of AfC or AfM

Table 4. Analysis of the ability of anti-IMDH B IgG to bind the surface of clinical isolates.

Strain Number	Original substratum	Pathogenicity (underlying disease):	Anti IMDH-B intensity	
			<u>Candida</u>	<u>Mycelium</u>
Isolate 46640	Human Lung	Aspergilloma	++	++
IHEM 1246	Outdoor air	-----	+	+
IHEM 2494	Human sputum	Allergic Bronchopulmonar Aspergillosis	++	++
IHEM 2739	Human sinus	Mycotic sinusitis	++++	++
IHEM 2895	Human bronchoaspiration (fungal ball)	Bronchitis	+++	+
IHEM 3007	Human lung	Pulmonary aspergillosis	-	+++
IHEM 4184	Human lung biopsy	Aspergillosis (heart transplant)	-	++
IHEM 4185	Human bone	Aspergillosis (heart transplant)	-	++
IHEM 4187	Human bronchial secretions	Aspergillosis (liver transplant)	+	+
IHEM 4699	Human bronchoaspiration	Aspergillosis (bone marrow transplant)	++	+
IHEM 4750	Human lung from autopsy	Aspergillosis (liver transplant)	+++	ND
IHEM 4756	Human sputum	Aspergillosis (marrow transplant)	-	+

Figure 1. The predicted protein sequences of CssI (A), hydrophobin (B), GAPDH-B (C), enolase (D), catalase B (E), catalase A(F), and isopropylmalate dehydrogenase B (G). X₁ is S or A and X₂ is L or I.

A

MLASFQFCILPRTYRTLLCSAGAGPLLIIQFVTVASALALAPTAVVARQGAAAFVTVNSIDVCPKKVAQEIIINPGPKVVTTTP
YTCDQVKLGHLGDLVSYYNFDIEPLTKDTFPYCKALKVFDNEGCLGFPTLWIPLESPLDKCIPEHYFSDEVKX₁SIFQLDCRE
DAPVKKEPYGPKGAEQSAPQAEHSTKQDAQQGSHQGGQEVQNSPKQEARQGSRPAAEAPKQEQEAEQASEAAPEKKASNPAD
SLGLGELTKVLGFR

B

VRFPVPDDITVKQATEKCGDQAQLSCCNKATYAGDVTIDIEGILAGTLKNLIGGGSGTEGLGLFNQCSKLDLQSPIIGIPIQ
DLVNQKCKQNIACCQNSPSDAVRFP

C

MATPKVGINGFGRIGRIVGLNSLSHGVDVVAVNDPFIIEVHYAAYMLKYDTHGQFKGTIETYDQGLIVNGKKIRFYAEKD
PSQIPWSETGAAYIVESTGVFTTKEKASAHKGGAKKVIISAPSADAPMFVMGVNNTTYTSDIQVLSNASCTTNCLAPLA
KVINDKFGIVEGLMTTVHSYTATQKVVDAPSNKDWRGRTAAQNIISSSTGAAKAVGKVIPLNGKLTGMAMRVPTSNVS
VVDLTCRLKKGASYDEIKQAIIKAASEEGELKNILGYTEDDVVSSDLNGDERSSIFDAKAGISLNPNFVKLVAWYDNEW

D

MPISKIHARSVYDSRGNPTVEVDVATETGLHRAIVPSGASTGQHEAHELRLDGDKTQWGGKGVLKAVKNVNETIGPALIKENI
DVKDQSKVDEFLNKLDTANKSNLGNAILGVSLAVAKAGAAEKGVPLYAHISDLAGTKKPYVLPVFPQNVNLGGSHAGGRL
AFQEFMIVPDSAPSFSEALRQGAEVYQKLKALAKKYGQSAGNVGDEGGVAPDIQTAEALDLITEAIEQAGYTGK
IKIAMDVASSEFYKADVKKYDLDFKNPESDPSKWLTYEQLADLYKSLAAKYPIVSIEDPFAEDDWEAWSYFYKTSDFQIVGD
DLTVTNPGRIKKAIELKSCNALLKVNQIGTLTESIQAAKDSYADNWGMVSHRSGETEDVTIADIAGVLRSGQIKTGAPCR
SERLAKLNQILRIEELGENTVYAGSKFRNAVNL

E

MRLTFIPSLIGVANAVCPYMTGELNRRDEISDGDAAAATEEFLSQYYLNDNDAMFMTSDVGGPIEDQNSLSAGERGPTLLEDF
IFRQKIQRFDHERVPERAVHARGAGAHGVFTSYGDFSNITAASFLAKEGKQTPVFVRFSTVAGSRGSSDLARDVHGFPATRFY
TDEGNFDIVGNIPVFFIQDAILFPDLIHAVKPRGDNEIPQAATAHDSAWDFFSQQPSTMTLLWAMSGHIGIPRSF
RHVDGFGVHTFRFVTTDDGASKLVKFHWKSLQGKASMWEEAQQTSGKNPDMRQDLHDAIEAGRYPEWELGVQIMDEEDQLR
FGFDLLDPTKIVPEEFVPIITKLGMQLNRNPNRYFAETEQVMFQPGHIVRGVDFTEDPLLQGRFVSYLDLTQLNRHGGPNFEQ
LPINQPRVPVHNNNRDAGQMFIPLNPHAYS PKTSVNGSPKQANQTVGDGFFTA PGRTTSGKLVRVAVSSSFEDVWS
QPRLFYNSLVPAAEQKFVIDAIRFENANVKSPPVVKNNVILQLNRIDNDLARRVARAIGVAEPEPDPTFYHNNKTADVGTFTGK
LKKLDGLKGVVLGSLVQHPGSVEGASTLRDLKDDGDVDVVLVAERLADGVDQTYSTSDAIQFDDAVVAAGAESLFAASFTTG
SANSASGASSLYPTGRPLQILIDGFRFGKTVGALGSGTAALRNAGIATSRDGVYVAQSVTDDFANDLKEGLRFTFKF
LDRFPVDH

F

MATKIAGGLHRAQEVLTQNTSSKSKKLVDLERDTADAHTQQPLTDDHGVRVSNTDQWLRVTNDRRTGPSLLEDQIAREKIHFR
DHERIPERVVHARGTGAFGNFKLKESEDLTAYAGVLTDTSRNTPVFVRFSTVQGSRGSDTVRDVRGFAVKFYTDEGNWDIV
GNIPVFFIQDAVKFPDFVHAVKPEPHNEVPQAQTAHNNFDFVYLHPEATHMFMWAMSDRAIPRSYRMMQGGFVN
TFALVNKEGKRHFVKFHWIPLHGVHSLVWDEALKLGGQDPDFHRKDLMEADNKAYPKWDFAIQVIPEEKQDDFEFDILDAT
KIWPENLVPLRVIGELELNRNVDEFFPQTEQVAFCTSHIVPGIDFTDDPLLQGRNFSYFDTQISRLGINWEELPINRPVCPV
LNHNRDGMRRHITQGTVNYWPNRFEAVPPTGKSGSGVGGGFTTYPQORVEGIKNRALNDKFRHHNQALFYNSMS
EHEKLHMKKAFSFLDHCDDPTVYERLAGHRLAETDLELAQKVAEMVGAPIPAKALKQNHGRRAPHLSTQTEFIPKNPTIASR
RIAIIGDGYDPVASTGLKTAIKAASALPFIIGTKRSAIYATEDKTSKGIIPDHHYDQGRSTMFDATFIPGGPHVATLRQN
GQIKYWISETFGHLKALGATGEAVDLVKETLSGTLHVQVASSQSPEPVEWYGVVTTAGGKQKPESFKESVQILKGAT
DFVGKFFYQISQHRNYQRELDGLASTIAF

G

MVTYTNILVLPDGDIGPEVMTAEAVKVLKVFENEHRKFNLRQELIGGCSIDAHGKSVTEEVKKALESDAVLFAAVGGPKW
DHIRRGDLGPEGGLLQLRKAMDIYANLRPCSASSPSASIAKEFSPPRQEVIEGVDFVVVRENCGGAYFGKKIEEDYAMD
EWGYSEREIQRITRLX₁AEX₂ALRHNPWPVVISLIDKANVLASSRLWRRVVEKTMTEYPPQVKLVHQLADSASLILATNPRALN
GVILADNTFGDMISDQAGSIVGTGLVLPASLDGLPSETRKRTNGLYEPHGSAPTIAQNIANPVMILCVALMFRYSLDM
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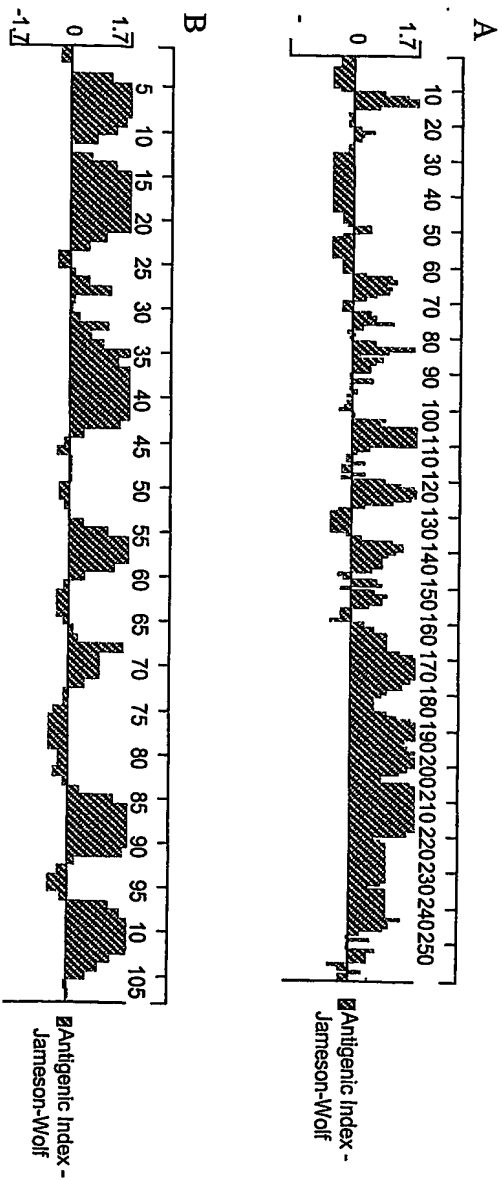


Figure 2. The predicted antigenicity indices of Csl (A) and hydrophobin (B) residues.

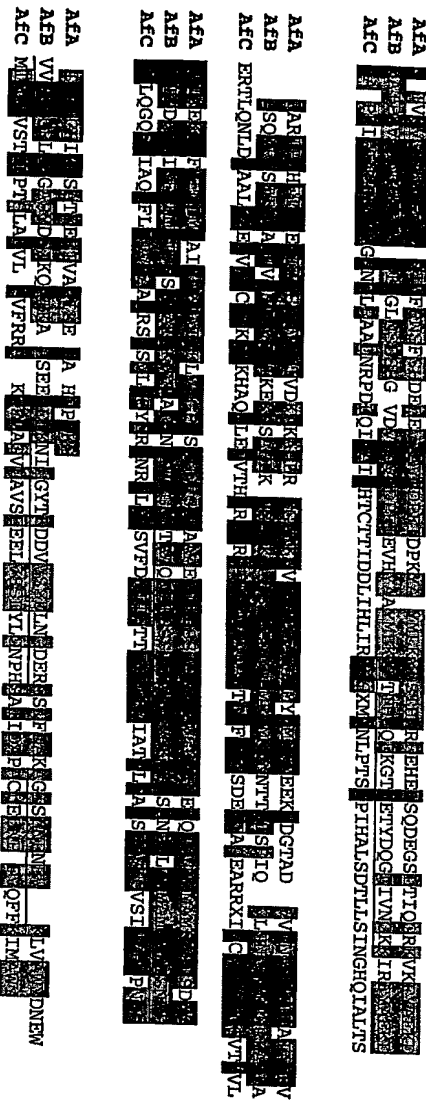


Fig. 4

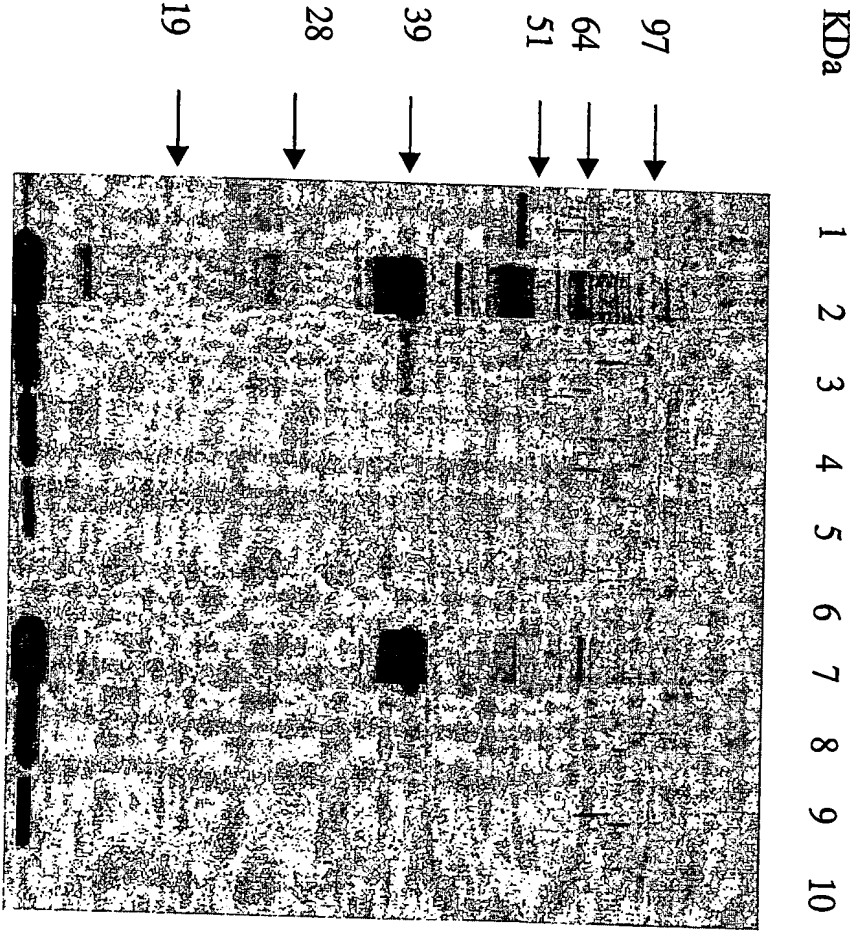


Fig. 5

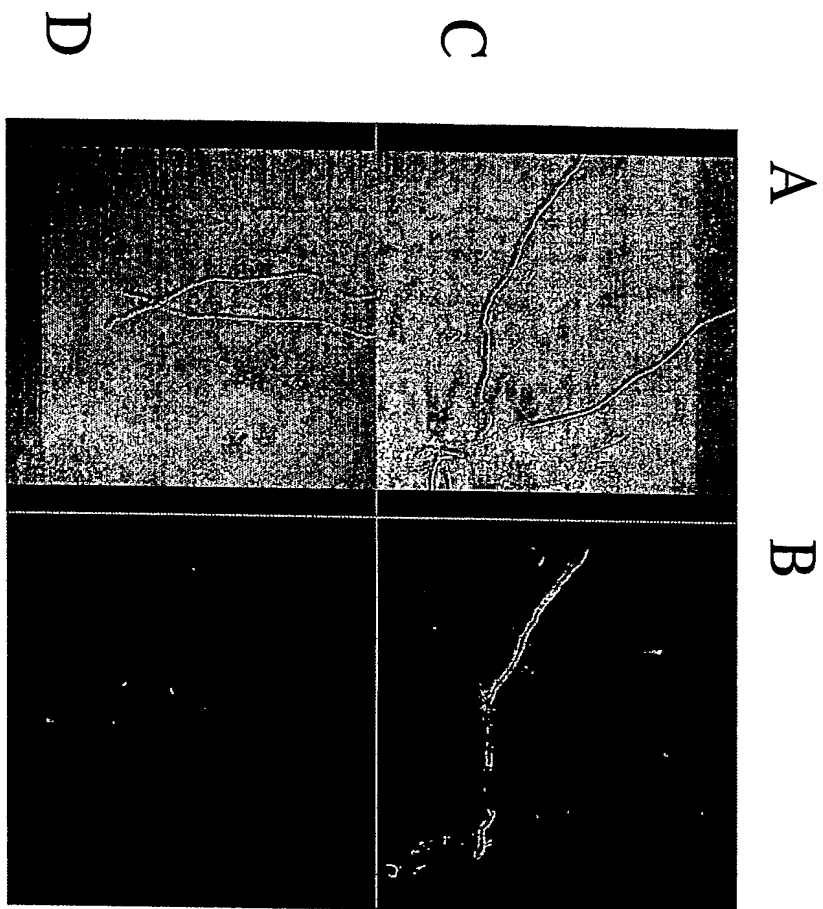
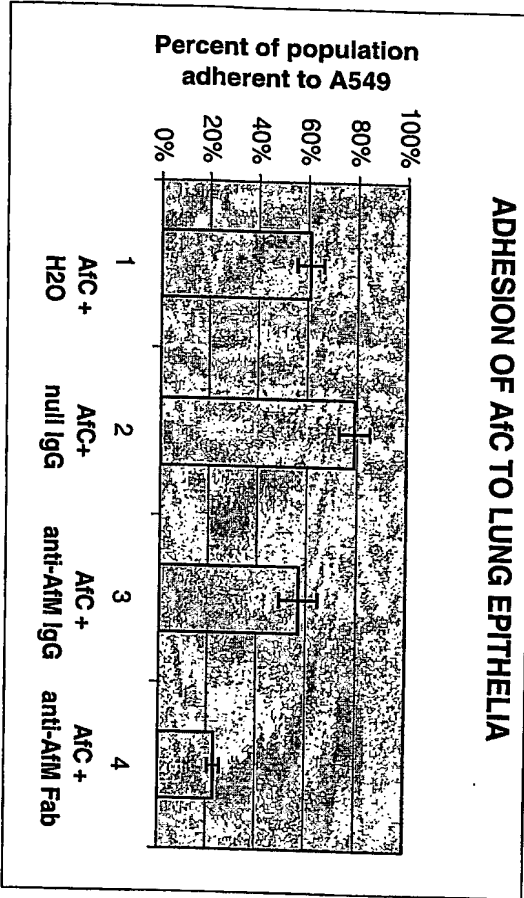
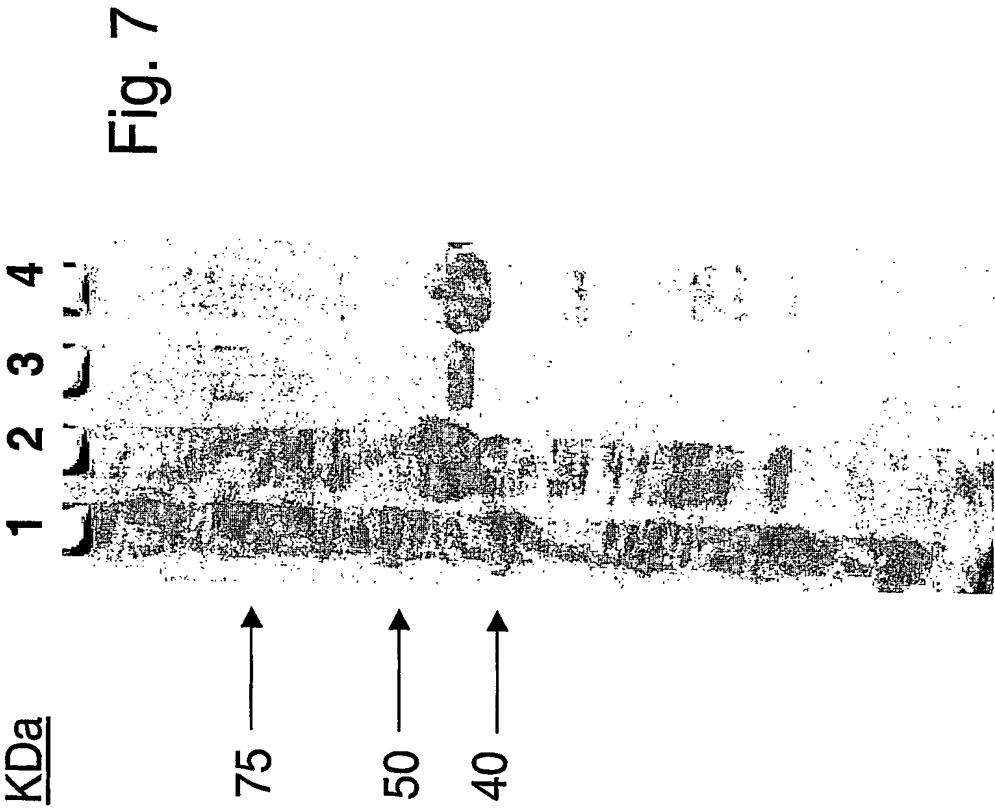


Figure 6





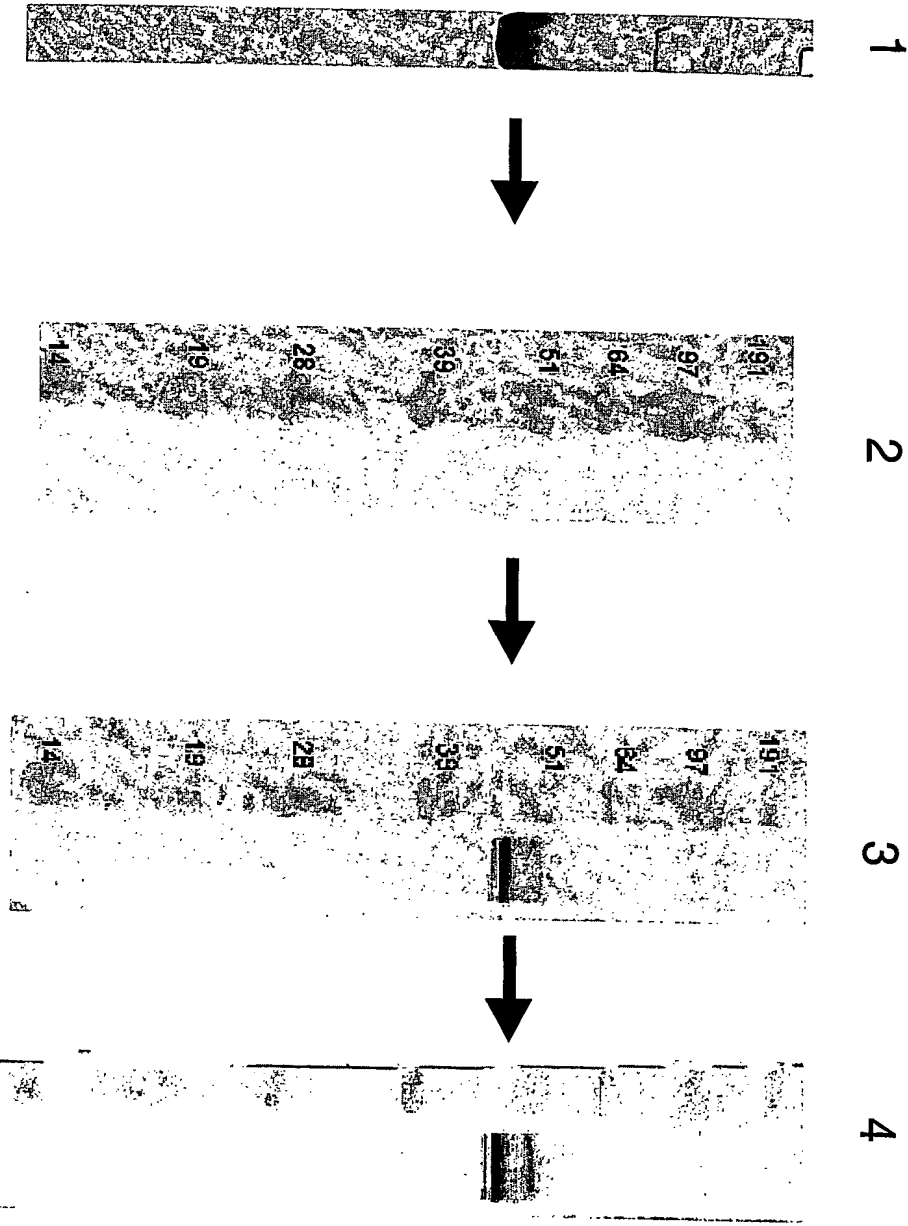
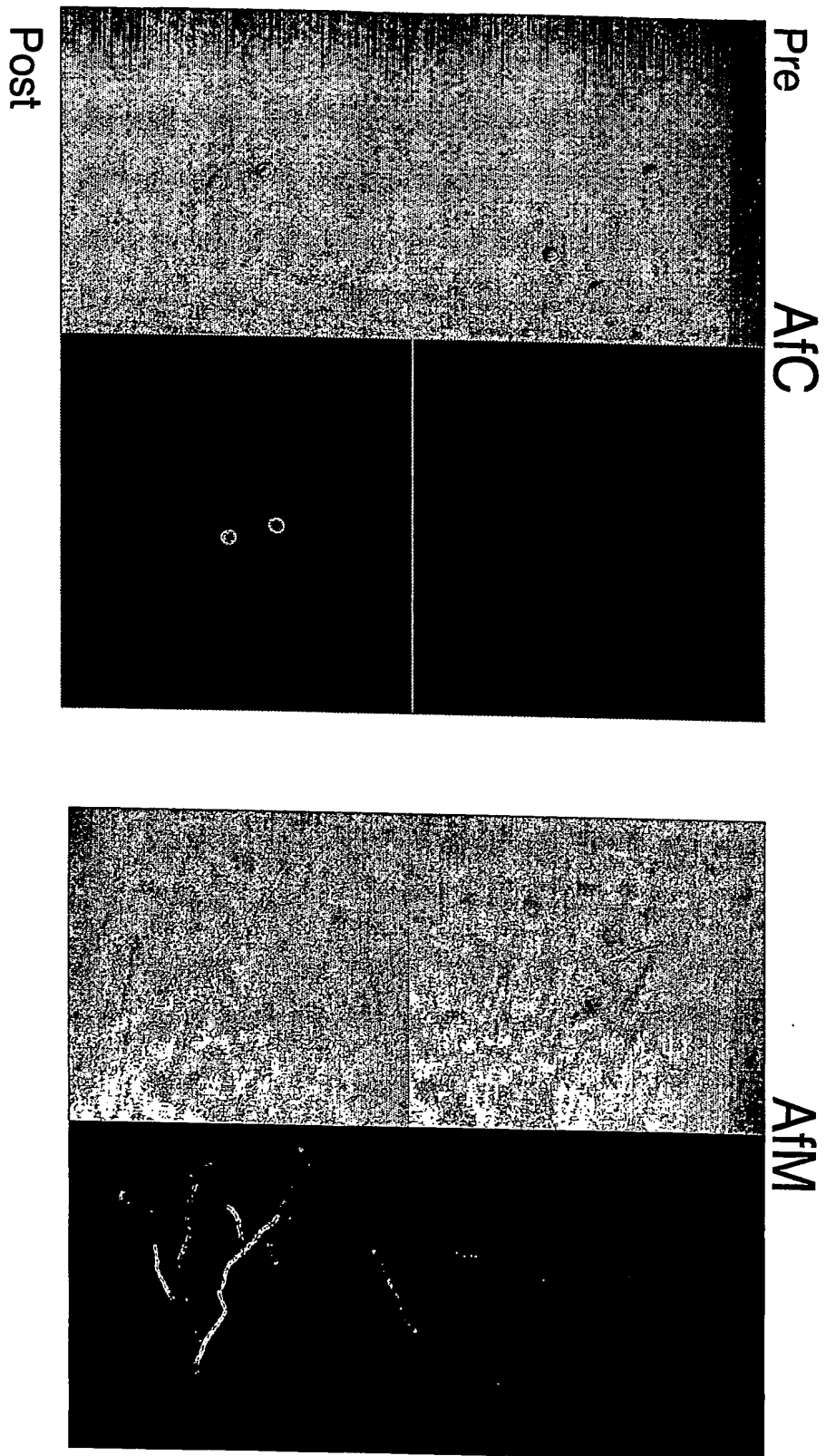


Fig. 8



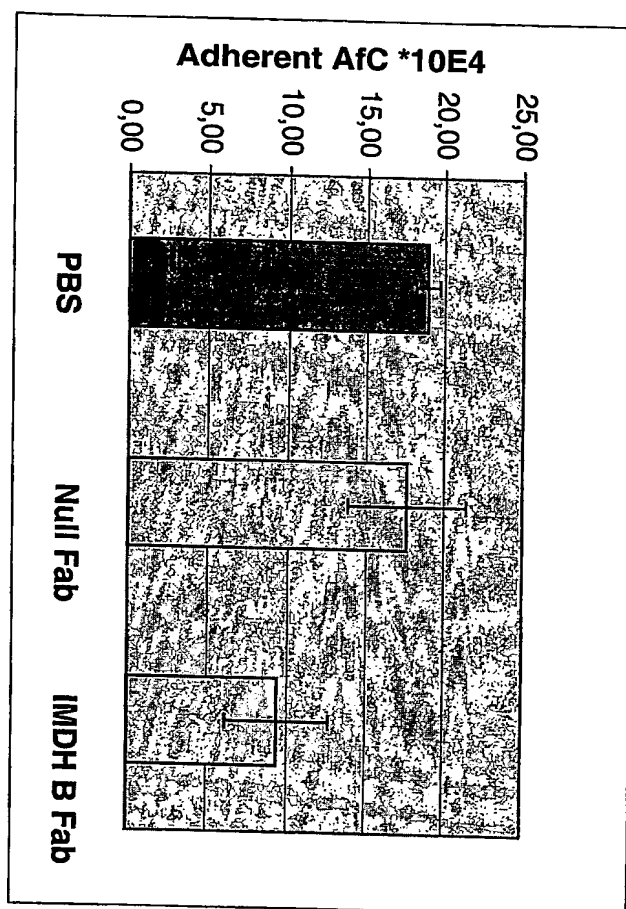


Fig. 10

Fig. 11

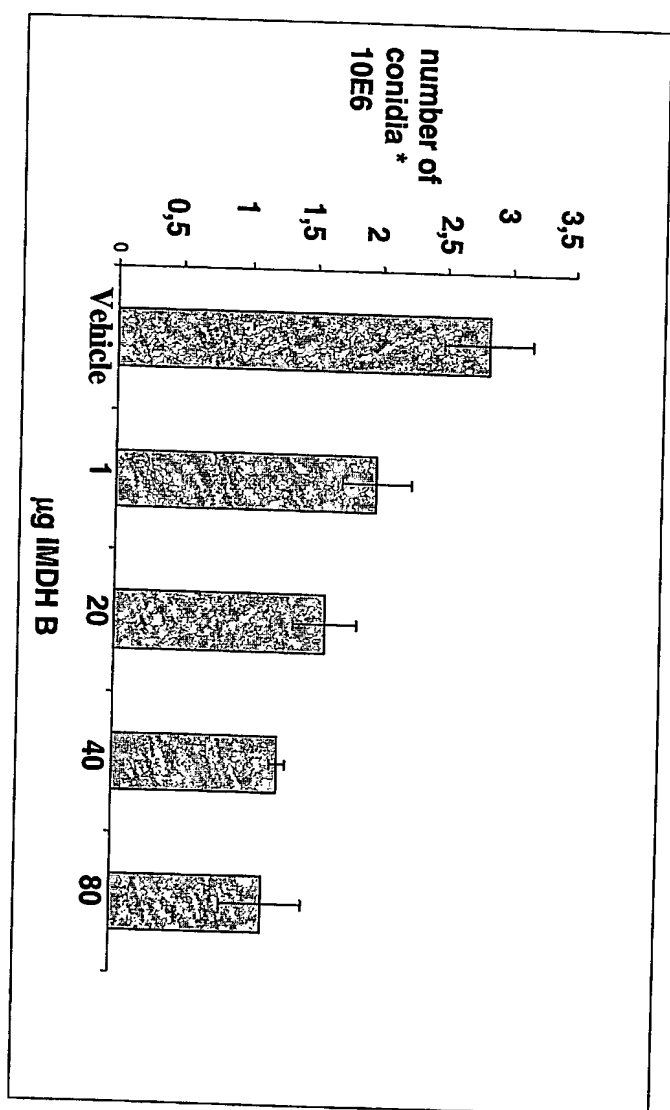


Figure 12

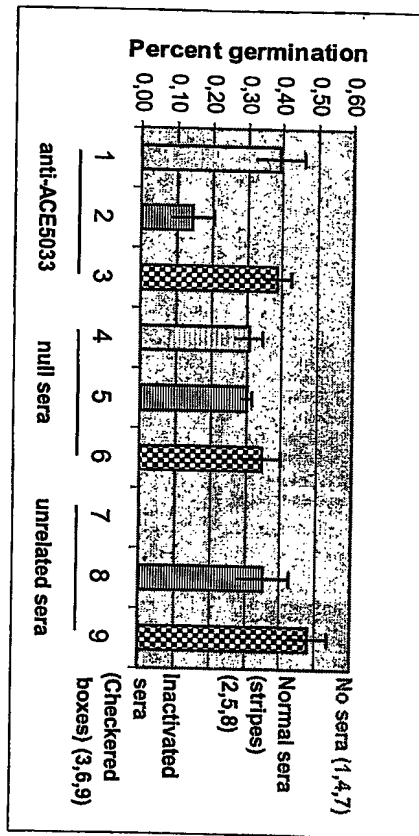


Figure 13

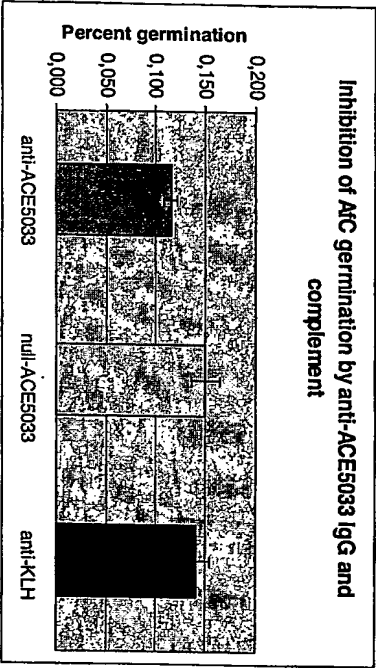


Fig. 14

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IMDHB1: 3 SYNIVVFAGDHCPEVSS----VLRVIEKCRDDATFNLQDQLLGGVSSIDATGSPLTDEA 58
      +YNI+V  GD  GPEV +    VL+V E   +    FNL+ +L+GG S IDA G  +T+E
IMDHB2: 4 TYNILVLPDGGIGPEVMTEAVKVLKVFEN--EHRKFNLRQELIGGCS-IDAHGKSVTEEV 60

IMDHB1: 59 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGLLRRLRKEMGTFGNLRPCNFAAPSLV-- 113
      AA  +DAVL  A+GGPKW    G   PE GLL+LRK M  + NLRPC+ ++PS
IMDHB2: 61 KKAALSDAVLFAAVGGPKWDHIRRGLDGPPEGGLQLRKAMDIYANLRPCSASSPSASIA 120

IMDHB1: 114 -DGSPLRPEVCRGVDFNIIRELTGGIYFGDRKEDDGSFGFAMDTEPYRAEIERITRLAAH 172
      + SP R EV  GVDF ++RE  GG YFG + E++   +AMD  YS  EI+RITRL+A
IMDHB2: 121 KEFSPFRQEVIEGVDFVVRRENCGGAYFGKKIEED--YAMDEWGYSEREIQRITRLSAE 178

IMDHB1: 173 LALQHNPPPLPVWSLDKANVLATSRLWRKTVTEVMAKEFPQLKVEHQLIDSAAMIMVKEPR 232
      +AL+HNPP PV  SLDKANVLA+SRLWR+ V + M  E+PQ+K+ HQL DSA++I+  PR
IMDHB2: 179 IALRHNPFPWPVISLDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLILATNPR 238

IMDHB1: 233 KLNGIVVTSNLFEDIISDEASVIPGSLGLLPSASLSGIP-DGKTKVNGIYEPHGSAPDI 291
      LNG+++  N FGD+ISD+A  I  G+LG+LPSASL G+P + + + NG+YEP HGSAP I
IMDHB2: 239 ALNGVILADNTFGDMISDQAGSIVGTLGVLPSASLDGLPSETRKRTNGLYEPHGSAPTI 298

IMDHB1: 292 AGKGIVNPVAAILSVAMMMQYSLNRMDDARAIEAVRNVIEAGIRTADIGGKSTTSEVGD 351
      AG+ I NPVA IL VA+M +YSL+   +A+ IE AV+ V++AGIRT D+GGKS T+EVGD
IMDHB2: 299 AGQNIANPVMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGD 358

IMDHB1: 352 AVAAELE 358
      A+ A L+
IMDHB2: 359 AIVAALQ 365

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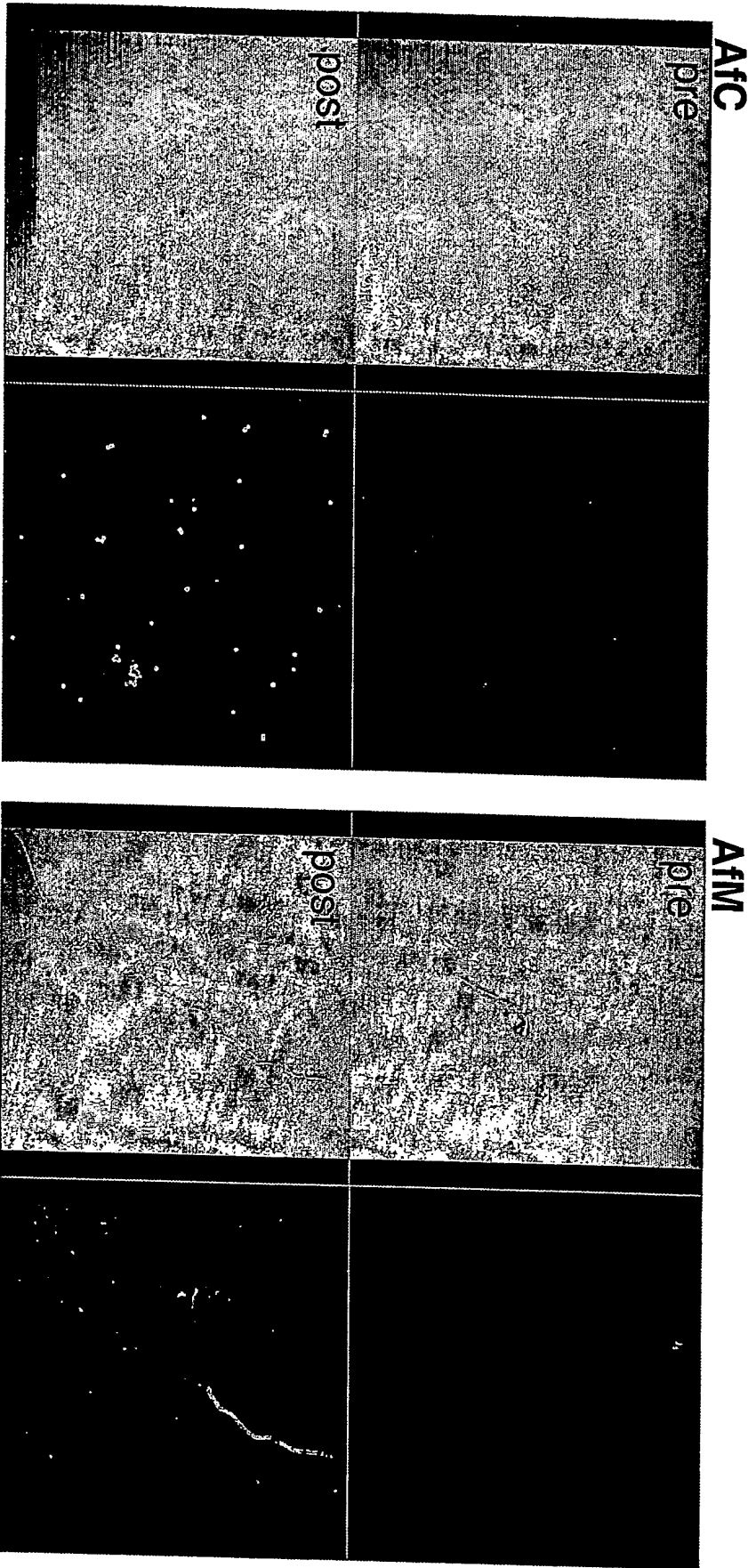
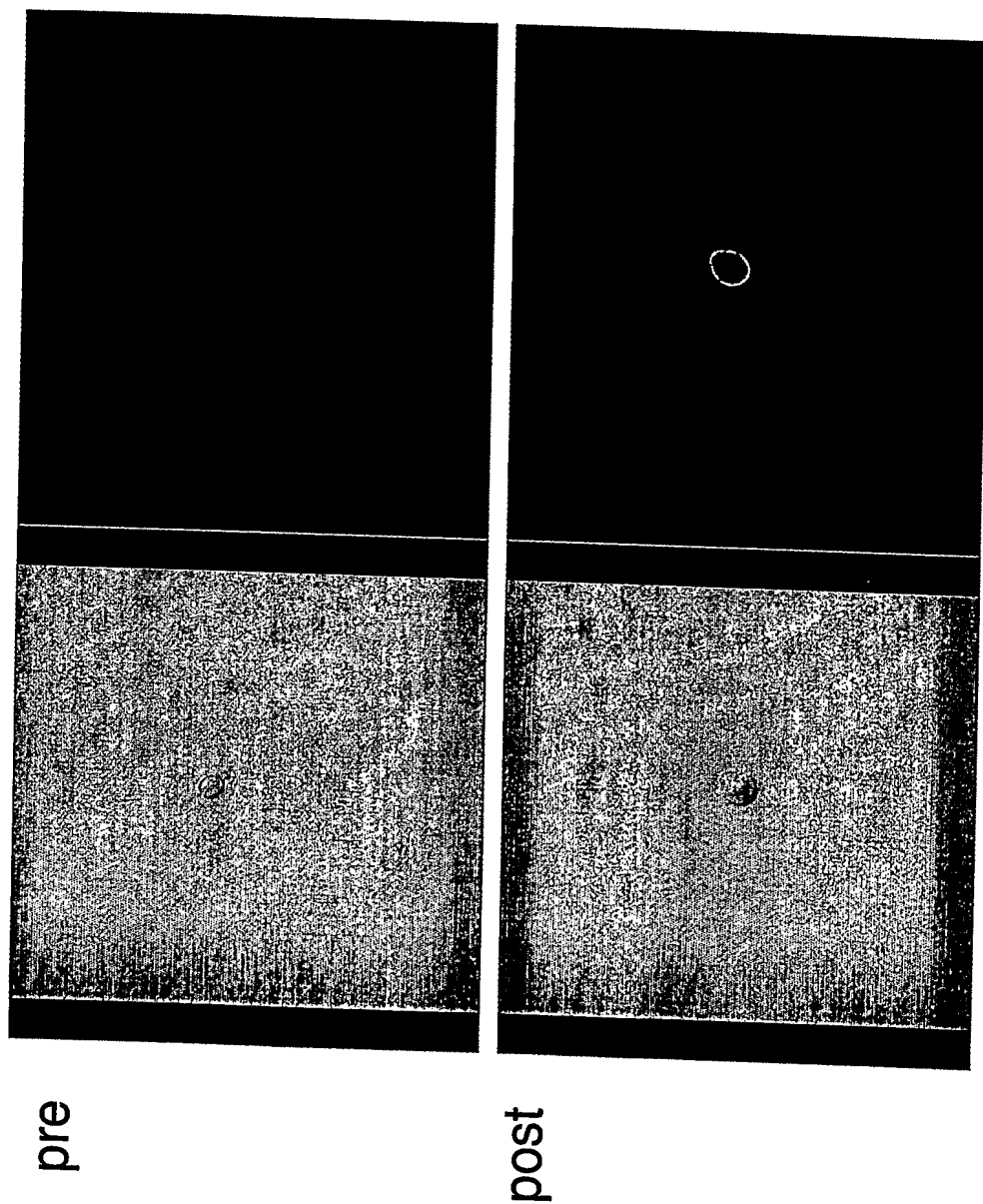


Fig. 15: Anti-GAP-B-2 (GAPDH)

Fig. 16
IHEM 3133



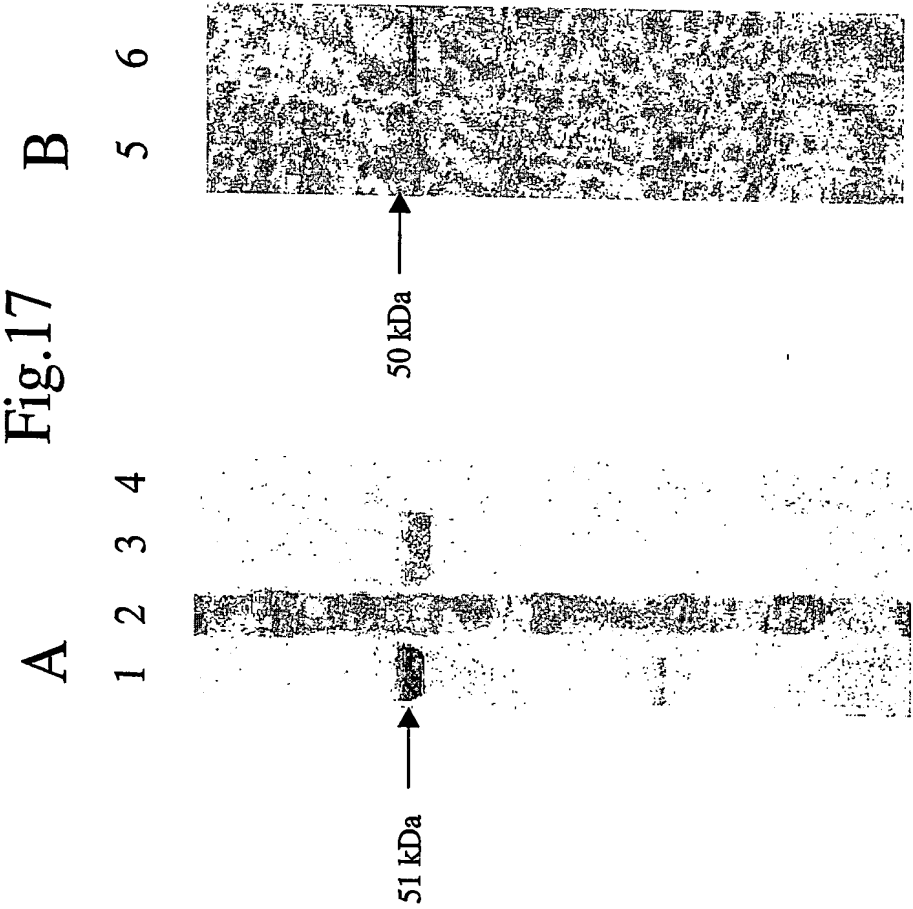


Figure 18**BLAST OF SEQ ID NO:36 AGAINST:**

Candida orf:

>orf19.7080 orf10262:179916-178795:e 1122 bp, 373 aa, contig 244073 bp
Length = 1122

Score = 335 bits (860), Expect = 1e-92

Identities = 185/368 (50%), Positives = 246/368 (66%), Gaps = 9/368 (2%)

Frame = +1

Query: 2 VTTYNILVLPDGGIGPEVMTEAVKVLKFEN----EHRKFNLQELIGGCSIDAHGKSVT 57
V T I VLPD +G E++ EA+KVLK E + +F+ + LIGG +IDA G +
Sbjct: 7 VKTKTITVLPGDHVGTEIVNEAIKVLKAIEAATPYQKIQFDFKHHLIGGAIDATGVPLP 186

Query: 58 EEVKKAALESDAVLFAAVGGPKWDHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPSA 117
++ ++A SDAVL AVGGPKW G PE GLL++RK +++YAN+RPC+ +S S
Sbjct: 187 DDALESASDAVLLGAVGGPKWG---TGTVRPEQGLLKIRKELNLYANIRPCNFASDSL 357

Query: 118 SIAKEFSPFRQEVIEGVDFVVVRENCGGAYFGKKIEEDY-----AMDEWGYSEREIQRI 172
E SP + EV++G + ++VRE GG YFG++ E+E+ A D Y+ E+ RI
Sbjct: 358 L---ELSPLKAEVVKGTNLIIVRELVGGIYFGERQEQEESDKKTAWDTEKYTVDEVTRI 528

Query: 173 TRLSAEIALRHNPPWPVISLIDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLI 232
TR++A +AL+HNPP P+ SLIDKANVLASSRLWR+ V+K ++ E+P + + HQL DSA++I
Sbjct: 529 TRMAAFMALQHNPPPLPIWSLIDKANVLASSRLWRKTVDKVISEFPALSVQHQLIDSAAMI 708

Query: 233 LATNPRALNGVILADNTFGDMISDQAGSIVGTLGVLPSASLDGLPSETRKRTNGLYEPH 292
L NP LNG+I+ N FGD+ISD+A I G+LG+LPSASL LP GLYEP H
Sbjct: 709 LIQNPTKLNGLIITSNMFGDIISDEASVIPGSLGLLPSASLASLPD--TNTAFGLYEPCH 882

Query: 293 GSAPTIAGQNIANPVAMILCVALMFRYSIDMETEAQRIEKAVQGVLDAGIRTPDLGGKSG 352
GSAP + N NP+A IL A M R SLD EA+ +E+AV+ VLD+GIRT DL G S
Sbjct: 883 GSAPDLPA-NKVNPIATILSAASMLRLSLDCVKEAEALEEAVKQVLDGIRTDLRGTSS 1059

Query: 353 TNEVGDAI 360
T EVGDAI
Sbjct: 1060TTEVGDAI 1083

Candida seq orf10262:179916-178795**1**

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QEQEESDKKTAWDTEKYTVDEVTRITRMAAFMALQHNPPPLPIWSLIDKANVLASSRLWRKTVDKVISEFPALS
VQHQLIDSAAMILIQNPTKLNGLIITSNMFGDIISDEASVIPGSLGLLPSASLASLPDNTNTAFGLYEPCHGSAP
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Figure 19**BLAST OF SEQ ID NO:36 AGAINST:**

Elrond pep

A. nidulans

>AnrP4374925 LE3B_ASPNG 3-isopropylmalate dehydrogenase B (Beta-IPM
dehyd
Length = 370

Score = 597 bits (1540), Expect = e-171

Identities = 295/364 (81%), Positives = 326/364 (89%), Gaps = 1/364 (0%)

Query: 4 TYNILVLPDGGIGPEVMTAEVKVLKVFENEHRKFNLRQELIGGCSIDAHGKSVTEEVKKA 63
+YNILVLPDGGIGPEVM EA K+L +F +F + ELIGGCSID HGKSVT+ V A
Sbjct: 5 SYNILVLPDGGIGPEVMAEATKILSLFNTSTVRFRTQTELIGGCSIDTHGKSVTQAVLDA 64

Query: 64 ALESDAVLFAAVGGPKWDHIRRGLDGPGEGLLQVRKAMDIYANLRPCSASSPSASIAKEF 123
A+ SDAVLFAAVGGPKWDHIRRGLDGPGEGLLQ+RKAMDIYANLRPCS SPS IA++F
Sbjct: 65 AVSSDAVLFAAVGGPKWDHIRRGLDGPGEGLLQVRKAMDIYANLRPCSVDSPSREIARDF 124

Query: 124 SPFRQEVIEGVDFVVVRENCGGAYFGKKIEEDDYAMDEWGYSEREIQRITRLSAEIALRH 183
SPFRQ+VIEGVDFVVVRENCGGAYFGKK+EE+DYAMDEWGYS EIQRITRLSAE+ALRH
Sbjct: 125 SPFRQDVIEGVDFVVVRENCGGAYFGKKVEEDDYAMDEWGYSASEIQRITRLSAELALRH 184

Query: 184 NPPWPVISLDBKANVLASSRLWRRVVEKTMTEYYPQVKLVHQLADSASLILATNPRLNGV 243
+PPWPVISLDBKANVLASSRLWRRVVEKTM+ EYPQVKLVHQLADSASLI+ATNPRLNGV
Sbjct: 185 DPPWPVISLDBKANVLASSRLWRRVVEKTMSEYYPQVKLVHQLADSASLIMATNPRLNGV 244

Query: 244 ILADNTFGDMISDQAGSIVGTGLGVLPSASLDGLPSE-TRKRTNGLYEPHGSAPTIGQN 302
ILADNTFGDM+SDQAGS+VGTGLGVLPSASLDGLP +++ +GLYEPHGSAPTIG+N
Sbjct: 245 ILADNTFGDMVSDQAGSLVGTGLGVLPSASLDGLPKPGEQRKVHGLYEPHGSAPTIGKN 304

Query: 303 IANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGDAIVA 362
IANP AMILCVALMFRYS +ME EA++IE AV+ VLD GIRT DLGG +GT E GDA+VA
Sbjct: 305 IANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTSDLGGSTGTREFGDAVVA 364

Query: 363 ALQG 366
AL+G
Sbjct: 365 ALKG 368

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ARDFSPFRQDVIEGVDFVVVRENCGGAYFGKKVEEDDYAMDEWGYSASEIQRITRLSAEL
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LNGVILADNTFGDMVSDQAGSLVGTGLGVLPSASLDGLPKPGEQRKVHGLYEPHGSAPTIG
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AVVAALKGEL

Figure 20**BLAST OF SEQ ID NO:36 AGAINST:**

BLASTP:temp_job2_pep_6_AnRP3711474
 >AnRP3711474 hypothetical protein [Aspergillus oryzae]
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Identities = 195/367 (53%), Positives = 260/367 (70%), Gaps = 10/367 (2%)

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 +++YNI+V GD GPEV EA+KVL+ E N FNL+ L+GG SIDA G +T+E
 Sbjct: 1 MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNRDVTNLDHLLGGASIDATGSPLTDEA 60

Query: 61 KKAALSDAVLFAAVGGPKWDHIRRLDGPGLLQLRKAMDIYANLRPCSASSPSASIA 120
 AA +DAVL A+GGPKW G PE G+L+LRK M + NLRPC+ ++PS
 Sbjct: 61 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLV-- 115

Query: 121 KEFSPFRQEVIEGVDFVVRNCGGAYFGKKIEBED--YAMDEWGYSEREIQRITRLSAE 178
 E SP R +V GV+F ++RE GG YFG++ E++ YAMD YS EI+RI RL+A
 Sbjct: 116 -ESSPLRADVCRGVNFNIIRELTGGIYFGERKEDDGSYGAMDEPYSRAEIERIIRLAH 174

Query: 179 IALRHNPWPVISLSDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLILATNPR 238
 +AL+H+PP PV SLDKANVLA+SRLWR+VV + M E+PQ+K+ HQL DSA++I+ NPR
 Sbjct: 175 LALQHDPPPLPVWSLDKANVLATSRLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPR 234

Query: 239 ALNGVILADNTFGDMISDQAGSIVGTLGVLPSASLDGLPSETRKRTNGLYEPHGSAPTI 298
 LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + NG+YEP HGSAP I
 Sbjct: 235 QLNGIVVTSNLFGDIIISDEASVIPGSLGLLPSASLSGIP-DGNSKVNGIYEPHGSAPDI 293

Query: 299 AGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGD 358
 AG+ I NPVA IL VA+M +YS + EA+ IE+AV V+++G+RT D+GGK+ T EVGD
 Sbjct: 294 AGKGIVNPVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGD 353

Query: 359 AIVAALQ 365
 A+ A L+
 Sbjct: 354 AVAAELE 360

Oryzae seq >AnRP3711474

MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNRDVTNLDHLLGGASIDATGSPLTDEA
 LNAAKNADAVLLGAIGGPKWGTGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLVESSPL
 RADVCRGVNFNIIRELTGGIYFGERKEDDGSYGAMDEPYSRAEIERIIRLAHLALQHD
 PPLPVWSLDKANVLATSRLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPRQLNGIV
 VTSNLFGDIIISDEASVIPGSLGLLPSASLSGIPDGNSKVNGIYEPHGSAPDIAGKGIVN
 PVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGDAAVAELE
 KLLK

Figure 21**BLAST OF SEQ ID NO:36 AGAINST:**

☐ BLASTP:temp_job2_pep_9_AnRP4379986
 >AnRP4379986 conserved hypothetical protein [Aspergillus nidulans
 FGSC A4
 Length = 357

Score = 149 bits (376), Expect = 1e-36
 Identities = 113/369 (30%), Positives = 186/369 (49%), Gaps = 27/369 (7%)

Query: 1 MVTTYNILVLPDGGIGPEVMTEAVKVLKVFENEHRKFNLRQELIGGCS--IDAHGKSVTE 58
 M TY I +P DGIGPEV+ V VLK ++ + F+L + S A GK + +
 Sbjct: 1 MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDWSSETFKATGKYIPD 60

Query: 59 EVKKAALSDAVLFAAVGGPKW-DHIRRGLDGPPEGGLQLRKAMDIYANLRPCSASSPSA 117
 + ++DA+LF AVG P DHI G L + + YAN+R P+
 Sbjct: 61 GGLEVLKKNDAILFGAVGAPDVPDHISLW-----GLRLAICQPFQQYANVR-----PTR 109

Query: 118 SIAKEFSPFRQEVIEGVDFVVRVRENCGGAYFGK-----KIEEEDYAMDEWGYSEREIQRI 172
 + SP R+ +D+V+VREN G Y G+ + + A + +S + ++RI
 Sbjct: 110 VLRGTQSPLRKCNTGDLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVERI 169

Query: 173 TRLSAEIALRHNPPWPVISLIDKANVLASSRLWRRVVEKTMTEYPOVKLVHQLADSASLI 232
 R + E A + P + + K+N + + V + ++P+V + L D+ +
 Sbjct: 170 MRFAFETAAR-RPRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTR 228

Query: 233 LATNPRALNGVILADNTFGDMISDQAGSIVGTGLGVLPASLDGLPSETRKRTNGLYEPTH 292
 + P +L+ I+A N D++SD A ++ G++G+ P+++LD ++ ++EP H
 Sbjct: 229 MVLKPESLD-TIVASNLHADILSDLAALAGSIGIAPTSNLD-----PTRQNPSMFEPH 282

Query: 293 GSAPTIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSG 352
 GSA I G+ IANPVA A M + L + A ++ + V+ V ++GI T DLGG +
 Sbjct: 283 GSAFDITGKGIANPVATFWTAAEMLEW-LGEKDAADKLMQCVESVCESGILTADLGGTAT 341

Query: 353 TNEVGDAIV 361
 T EV A+V
 Sbjct: 342 TKEVTSADV 350

Nidulans seq >AnRP4379986

MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDWSSETFKATGKYIPD
 GGLEVLKKNDAILFGAVGAPDVPDHISLWGLRLAICQPFQQYANVRPTRVLRGTQSPLRK
 CNTGDLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVERIMRFAFETAAR
 PRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTRMVLKPESLDTIV
 ASNLHADILSDLAALAGSIGIAPTSNLDPTRQNPSMFEPHGSAGFDITGKGIANPVATF
 WTAAEMLEWLGEKDAADKLMQCVESVCESGILTADLGGTATTKEVTSADVVEINRLN

Figure 22**BLAST OF SEQ ID NO:36 AGAINST:**

>gnl|TIGR_222929|contig:1772:c_posadasii *Coccidioides posadasii* C735
 unfinished fragment of genome
 Length = 119053

Score = 286 bits (732), Expect(2) = e-128

Identities = 146/233 (62%), Positives = 173/233 (74%), Gaps = 24/233 (10%)

Frame = -3

Query: 160 AMDEWGYSTTEIQXXXXXXXXXXXXHDPWPVISLTKANVLASSRLWRRVVENTISVEYP 219
 AMDEWGYST E+Q HDPPWPVIS+DKANVLASSRLWRRVVE T++ E+P
 Sbjct: 33806 AMDEWGYSTQEVQRIARLAHVALRHDPWPVISMDKANVLASSRLWRRVVEKTLTTEFP
 33627

Query: 220 QVKLVHQLADSASLIMATDPRVLNGVILADNTFGDMLSDQAGSLIGTLGVLPASLDGLP 279
 QVK HQLADSASLIMAT+PR LNGV+LADNTFGDMLSDQAGS++G+LGVLPASL G+P
 Sbjct: 33626 QVKFSHQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLPASLSGIP
 33447

Query: 280 HPGKQE--KVRGLYEPHGSAPT-----IAGKNIANPTAMILC 315
 +++ K LYEPHGSAPT IAGKN+ANP AMILC
 Sbjct: 33446 GEKRKDGKKSALYEPHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILC
 33267

Query: 316 VSLMFRYSFNMENEARQIEDAVRAVLDRGLRTPDLGGNSSTQEFDAVVAALQ 368
 V++MFRYSFNME EA+ IE+AV A L+ G+RTPDLGG + T + G+A+VA ++
 Sbjct: 33266 VAMMFRYSFNMEEPAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHIK 33108

Query: 4 TRAYNILVLPDGGIGPEVMAEAIKVLRTFNSSSMQFHLQEELIGGISIDTHGHSVTQPPX 63
 ++ YNIL LPGDGIGPE+MAEAIKVL+ F+S ++ F+L+ ELIGG SID HG +T
 Sbjct: 34383 SKTYNILTLPDGGIGPEIMAEAIKVLQAFSSPNLNFNLRLNELIGGCSIDAHGTPITDAVK
 34204

Query: 64 XXXXXXXXXXXXXXXGGSKVDHIRRGLDGPGEGLLQVRKAMDIYANLRPCSVDVPSREIAR 123
 GG K D RRGL+GPEGGLLQ+RK +D+Y N+RPCS DV ++R
 Sbjct: 34203 QAALSDAVLFASVGGPKWDSSRRGLEGPGEGLLQLRKVLDVYGNVPCSTDV-CASVSR
 34027

Query: 124 DFSPFRQEVIEGVDFVVFVRENCGGAYFGKKVEEENY 159
 +FSP+R EV+EGVDFVVF+RENCGGAYFGK VE+E+Y
 Sbjct: 34026 EFSPYRTEVVEGVDFVVFVRENCGGAYFGKXVEDEDY 33919

Coccidioides

2

SKTYNILTLPDGGIGPEIMAEAIKVLQAFSSPNLNFNLRLNELIGGCSIDAHGTPITDAVKQAALSDAVL
 FASVGGPKWDSSRRGLEGPGEGLLQLRKVLDVYGNVPCSTDVCASVSREFSPYRTEVVEGVDFV
 VLRENCGGAYFGKXVEDEDYAMDEWGYSTQEVQRIARLAHVALRHDPWPVISMDKANVLASSR
 LWRRVVEKTLTTEFPQVKFSHQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLP
 SASLSGIPGEKRKDGKKSALYEPHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILC
 VAMMFRYSFNMEEPAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHIK

Figure 23 SEQ ID NO:36 against: Cryptococcus >chr01b.b3501.031220.C11
(289426 bp) Length = 289426

Score = 183 bits (465), Expect(3) = 3e-68 Frame = +3
Identities = 113/258 (43%), Positives = 144/258 (55%), Gaps = 39/258 (15%)

```

Query: 148      FGKKIE--EEDYAMDEWGYSEREIQRITRLSAETALRHNPFPWFVISLTKANVLASSRLWR 205
               FG++ E +E A D+ YS+ EI+RITR++A+IAL PP P+ S+DKANVLA+SRLWR
Sbjct: 173334   FGERQETNDEGVAWDQCIYSKPEIERITRVAAQIALAAEPPLPITSVDKANVLATSRLWR 173513

Query: 206      RVVEKTMTEYPQVKLVHQLADSASLILATNPRLNGVILADNTFGDM----- 253
               + V + M EYPQ+KL HQL DSA++I+ NPR LNGV+L +N FGDM
Sbjct: 173514   KTVSELMAKEYPQLKLEHQLVDSAAMIMIANPRKLNGLVLLTENMFGDM*VLSMVTKYRC* 173693

Query: 254      -----ISDQAGSIVGTGLVLPASLDGLPSETRKRTNGLYE-----PTHGS 294
               S A + L + P LP ++ HGS
Sbjct: 173694   VCVVFLTKAPSSPAPLVSSLLRLSPVPPTLSLPPVWMSRSTIFPFLTYPN*PLCSIHGS 173873

Query: 295      APTIAGQNIANPVMILCVALMFRYSLDMETEAQRIEKAVQGVLDAG-----IRTPDLG 348
               AP IAGQ IANP+ IL A+M RYSL EA IE+AVQ VLD+ RT DLG
Sbjct: 173874   APDIAGQGIANPIGTILSAAMMLRYSLSGKGREALIEQAVQKVLDSEAESGGFDYRTKDLG 174053

Query: 349      GKSGTNEVGDAIVAALQG 366
               G+ T EVGD +V L+G
Sbjct: 174054   GQRSTKEVGDKVVEVLKG 174107

Query: 15       IGPEVMTEAVKVLKFENEHR-KFNLRQELIGGCSIDAHGKSVTEEVKKALESDAVLFA 73
               IGPEV+ EAV+VL+ N K +L+ GG +ID HG + +E KA E+DAVL
Sbjct: 172844   IGPEVVAEAVRVLETIVNHSCLKLDLKSDFGGAAIDNHGVPLPDETLKACKEADAVLMG 173023

Query: 74       A-----VGGPKWDHIRGLDGPEGGLQLRKAMDIYANLRPCSASSPS 116
               A VGGPKW G PE G+L+LRK + +YAN+RP A+ S
Sbjct: 173024   ACDFLAIRIKS*TA*KGSVGGPKWGV---GPNRPEQGILKLRKELGLYANIRP--ANFAS 173188

Query: 117      ASIAKEFSPFRQEVIEGVDFVVRVRENCGG 145
               S+ K SP +++ G D +V+RE GG
Sbjct: 173189   ESLLKR-SPLKEDTARGTDIIVLRELIGG 173272

Query: 244      ILADNTFGDMISDQAGSIVGTGLVLPASLD-----GLPS---ETRKRTNGLYEPH 292
               +L + +GD++SD + ++G LG+ PS ++ G PS K ++E H
Sbjct: 238292   LLIPHRYGDILSDLSAGLIGGLGLTPSGNIGKVSLSHDYGSPSIELTGDK*DASIFEAVH 238471

Query: 293      GSAPTIAQNIANPVMILCVALMFR----- 318
               GSAP I G+ +ANP A++L +M R
Sbjct: 238472   GSAPDIEGKGLANPTALLSSLMMLR*VTQIPSVIVPALYPSVPDHTHPLARNVADLFVH 238651

Query: 319      YSLDMETEAQRIEKA---VQG-----VLDAGIRTPDLGGKSGTNEVG 358
               + + A +IEKA V G + + T DLGK+GT E D
Sbjct: 238652   RHMSLYELADKIEKAALSVSGTFPWLFTFEMLIQVS*TIAEGKAITRD LGGKAGTKEYTD 238831

Query: 359      AIVAAL 364
               AI++ L
Sbjct: 238832   AILSKL 238849

Query: 95       LQLRKAMDIYANLRPCSASSPSASIAKEFSPFRQEVIEGVDFVVRVRENCGGAYFGKKIEE 154
               L LR+ ++AN+RPC SI +P+ + V+ V++REN G Y G IE
Sbjct: 237609   LTLRRTFSLFANVRP-----VSIKGYKTPY-----DNVNTVLIRENTEGEYSG---IEH 237749

Query: 155      E 155
               E
Sbjct: 237750   E 237752

Query: 5        YNILVLPDGGIGPEVMEAVKVLK 28
               Y + ++PGDGIGPE+ ++ K
Sbjct: 237256   YTVTLIPDGGIGPEIANSVKQIFK 237327

Query: 4        TYNILVLPDGGIG 16
               ++ I VLPDGGIG
Sbjct: 172752   SFKITVLPDGGIG 172790

```

Clustalw of sequences of figure 18-22

```

! Sequence: BLASTP:temp_job2_pep_4_AnRP4374925          nidulans (see figure 19)
! Sequence: BLASTP:temp_job2_pep_6_AnRP3711474          oryzae (see figure 20)
! Sequence: BLASTP:temp_job2_pep_9_AnRP4379986          nidulans (see figure 21)
! Sequence: USERPROTEIN:1_job6_1                       candida (see figure 18)
! Sequence: USERPROTEIN:2_job7_2                       coccidioides (see figure 22)
CLUSTAL W (1.82) multiple sequence alignment

temp_job2_pep_4_AnRP4374925      ---SYNILVLPDGGIGPEVMAEATKILSLFNTST-----VRFRTQTTELIGG
temp_job2_pep_6_AnRP3711474      -MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNR----DVTFNLDHLLGG
temp_job2_pep_9_AnRP4379986      MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQS--FSLDFTHLDWSS
1_job6_1                         -VKTKTITVLPGDHVGTEIVNEAIKVLKAIEAATPYOKIQDFDKHHLIGG
2_job7_2                         -SKTYNILLTPDGGIGPEIMAEAIKVLQAFSSPN----LNFNLRLNELIGG
                                   :  *  .  .  *  *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
                                   :  *  .  .  *  *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

temp_job2_pep_4_AnRP4374925      CSIDTHGKSVTQAVLDAAVSSDAVLFAAVGGPKWDHRRGLDGPESGLLQ
temp_job2_pep_6_AnRP3711474      ASIDATGSLTDEALNAAKNADAVLIGAIGPKWG---TGAVRPEQGILK
temp_job2_pep_9_AnRP4379986      ETFKATGKYPDGGLEVLKKNDAILFGAVGAPDVP----DHISLWGLRLA
1_job6_1                         AAI DATGVLPDDDALESAKSSDAVLLGAVGGPKWG---TGTVRPEQGILLK
2_job7_2                         CSIDAHGTFITDAVKQAALLESDAVLFAVGGPKWDSRRRGLGEGEGGLLQ
                                   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
                                   :  *  .  .  *  *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

temp_job2_pep_4_AnRP4374925      VRKAMDIYANLRPCSVDSPSREIARDFSPFRQDVIEGDFVWVRENCGGA
temp_job2_pep_6_AnRP3711474      LRKEMGTFGNLRPCNFAAPSL----VSSPLRADVCRCGVNFNIIRELTGGI
temp_job2_pep_9_AnRP4379986      ICQFPQQYANVRPTRLRGTHQ-----SPLRKCNCTGLDWDWIVRENSEGE
1_job6_1                         IRKELNLIYANIRPCNFASDSL---LELSPLKAEVVKGNLIIVRELVGGI
2_job7_2                         LRKVLVDVYGNVRPCSTDVCAS-VSREFSPYRTEVVEGVDFVVLRENCGGA
                                   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
                                   :  *  .  .  *  *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

temp_job2_pep_4_AnRP4374925      YFG-----KKVEEDDYAMDEWGYSAEIQIRITRLSAELALRHDPWPVVIS
temp_job2_pep_6_AnRP3711474      YFGERKEDDGS-----YAMDTEPYSAEIERIIRLAAHLALQHDPPLPWMS
temp_job2_pep_9_AnRP4379986      YAGQGRSHRGHPWEVATEVAIFSRQGVFERIMRFAFETAAGR-PRKILLTV
1_job6_1                         YFGERQEQEESDKTAWDTEKYTVDEVTRITRMAAFMALQHNPPLPWIS
2_job7_2                         YFG-----KKVEDEDYAMDEWGYSTQEVQRIARLAAHVALRHDPWPVVIS
                                   *  *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
                                   :  *  .  .  *  *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

```

Figure 25 Continuation from figure 24

```
temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

LDKANVLASSRLWRRVVEKTMSEEPQVKLVHQLADSLIMATNPRALN
LDKANVLATSLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPRQLN
VTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTRVLKPESLD
LDKANVLASSRLWRKTVDKVISEEFPALSVQHQLIDSAAMILIQNPTKLN
MDKANVLASSRLWRRVVEKTLTTEFPQVKFVSHQLADSLIMATNPRSLN
: ** . . . * : : : * : : * : : * : : * : : * :
GVLLADNTFGDMVSDQAGSLVGTGLVLPASLDGLP--KPGEQKVVHGLY
GIVVTSNLFGDIISDEASVIPGSLGLLPASLSGIP----DGNSKVNGIY
-TIVASNLHADILSDLAALAGSIGIAPTNSLDPTR-----QNPSMF
GIITSNMFGDIIISDEASVIPGSLGLLPASLASLP----DTN-TAFGLY
GVLLADNTFGDMLSDQAGSIVGSLGVLPSASLSGIPGEKRRKDGKKSALY
: : : * . . . * : : * : : * : : * : : * : :
EPTHGSAPTIAGKNIANPTAMILCVLMFRYSFNMEAEARQIEAAVRTVL
EPIHGSAFDIAGKIVNPVAAILSVAMMQYSFGLFAEARAIEQAVSNVI
EPIHGSAFDITGKIANPVATFWTAAEMLEWLGEKDAADKLMQCVCESVC
EPCHGSAPDLPAN-KVNPIATILSAA SMLRLSLDCVKEAEALEEAVKQVL
EPTHGSAPT-----
** ****

DKGIRTSDLGGSTGTREFGDVAVVAAKKG
ESGVRTGDIGGKATTAEVGDVAAAELE-
ESGILTADLGGTATTKEVTSVV-----
DSGIRTADLRGTSSTTEVGDAI-----
```